

Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6%, 60C, Long Gel)

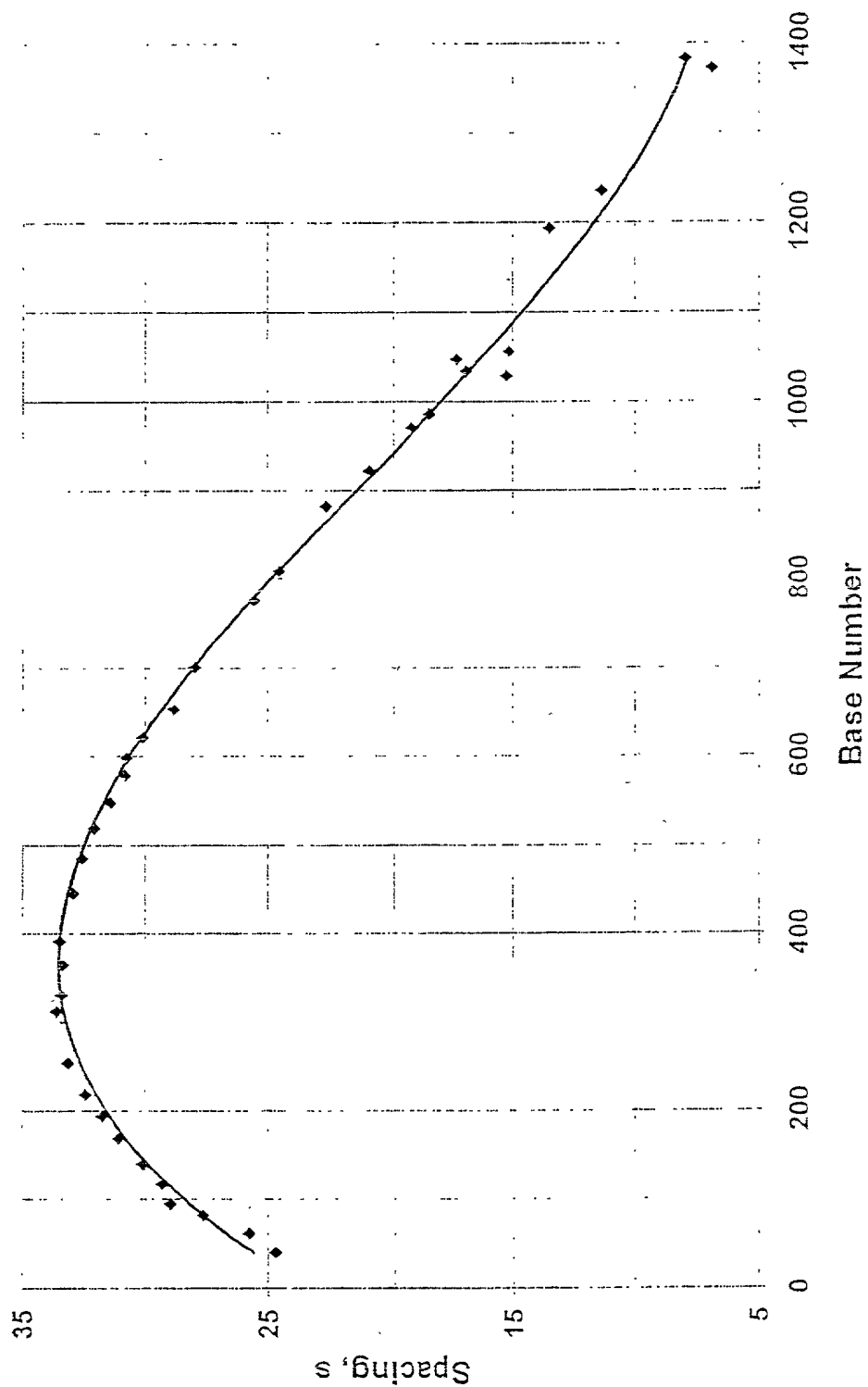


Figure 1

Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
(M13, Long Gel, 55C, T=6%)

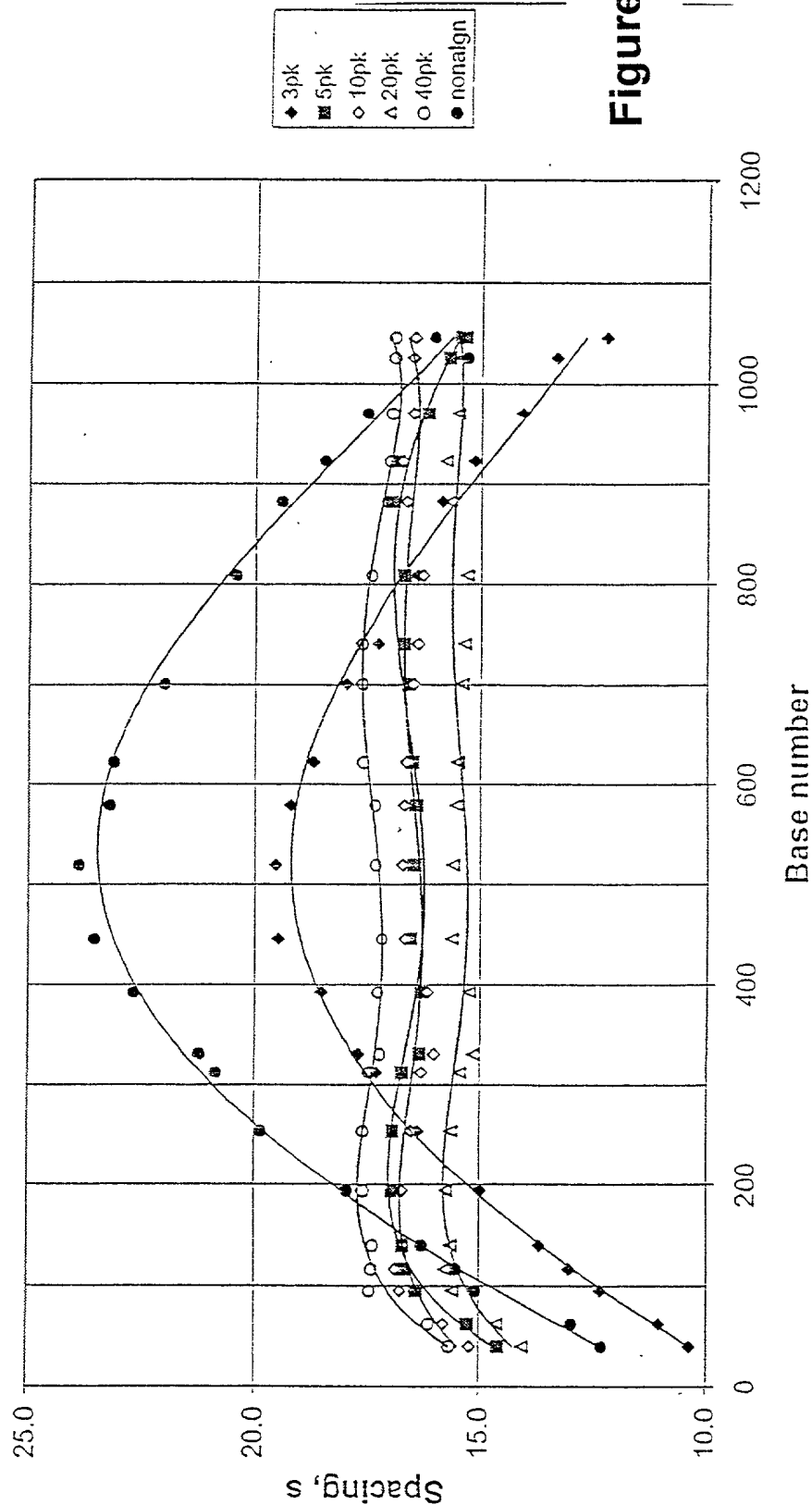


Figure 2

Standard Deviation (%) of the Spacing Between Adjacent Bases from
Average as a Function of Number of Peaks Used as a Reference for
Alignment of Raw Data

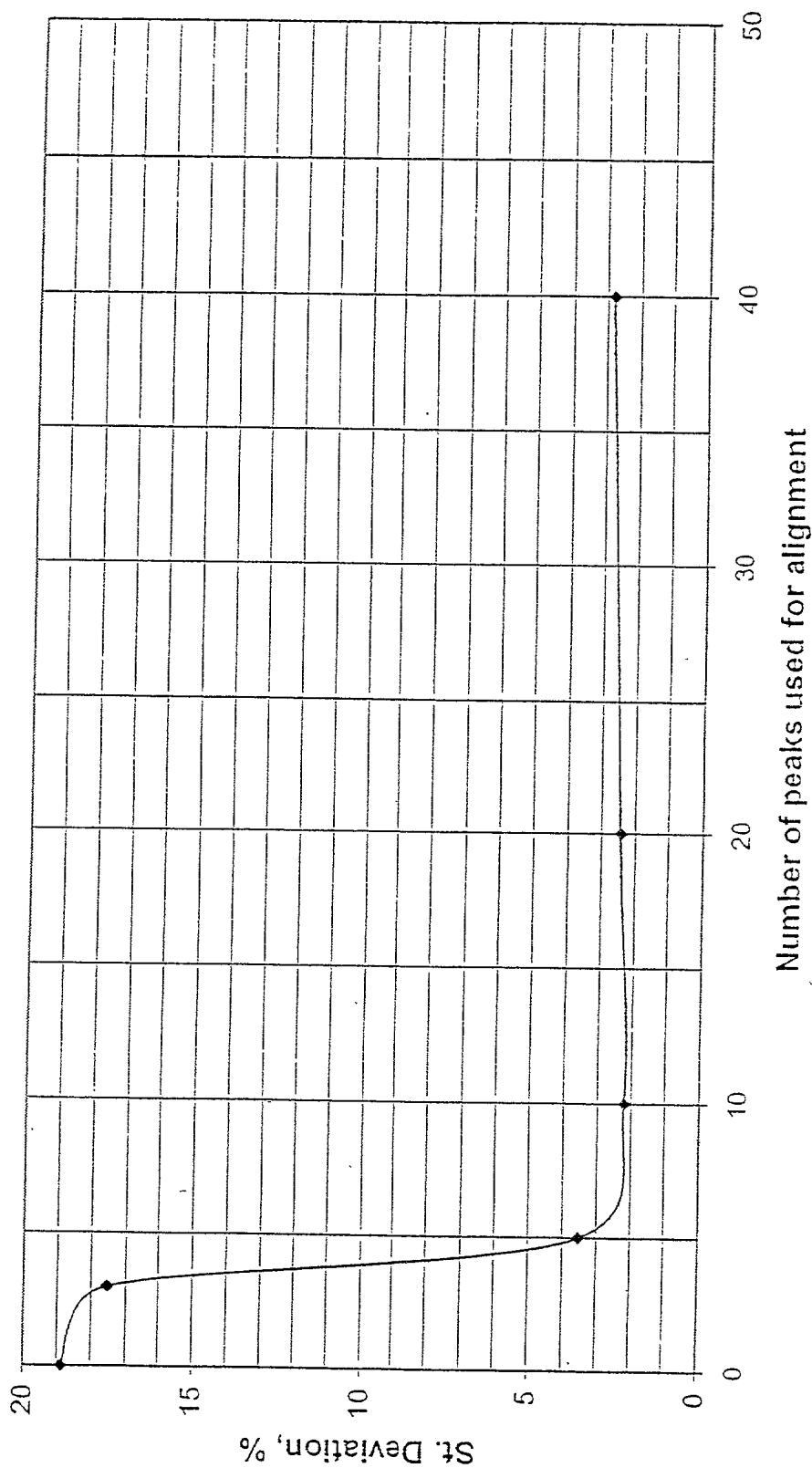
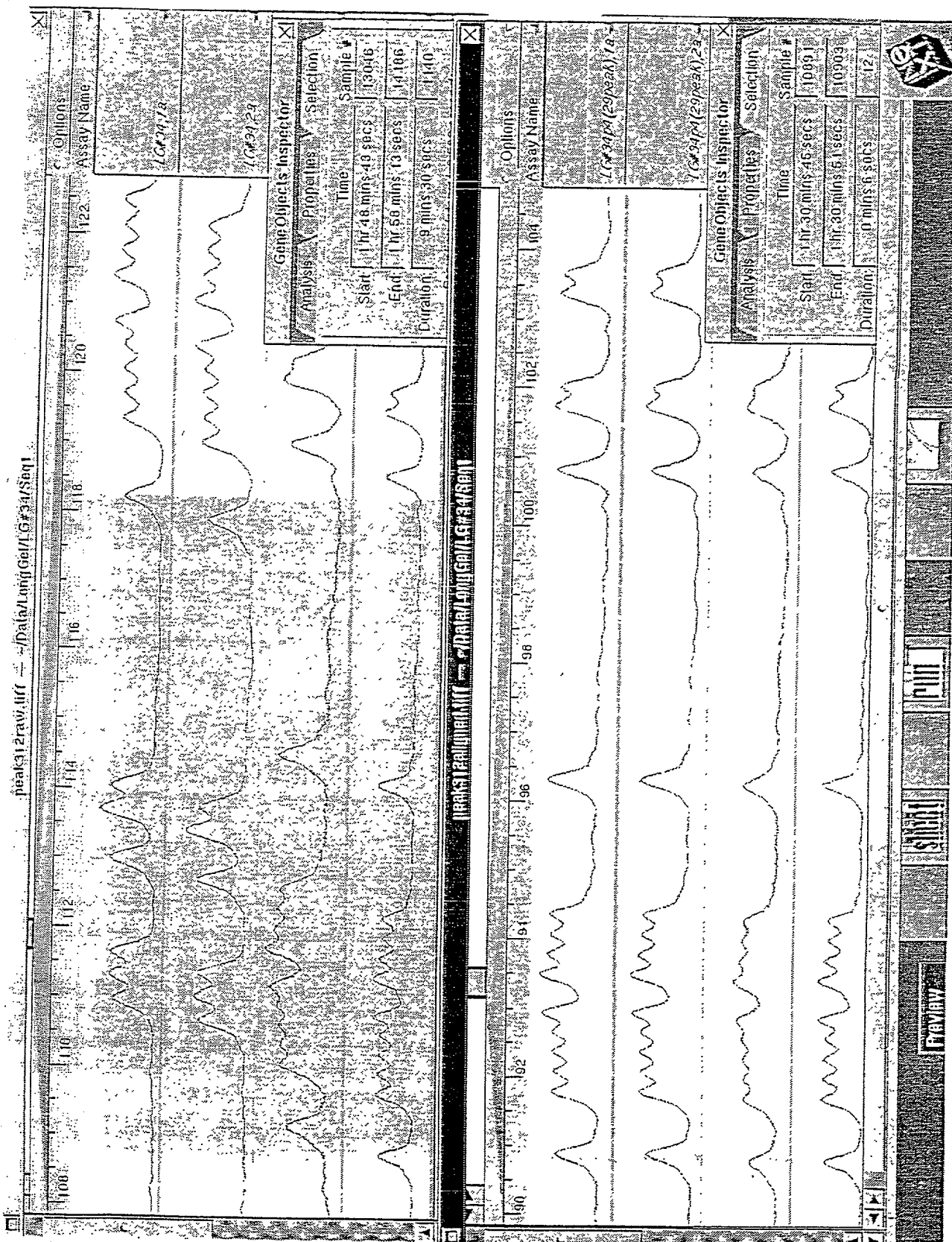


Figure 3

peak312raw.tif -- ~/Data/LongGel/LG#34/Seq1



Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)

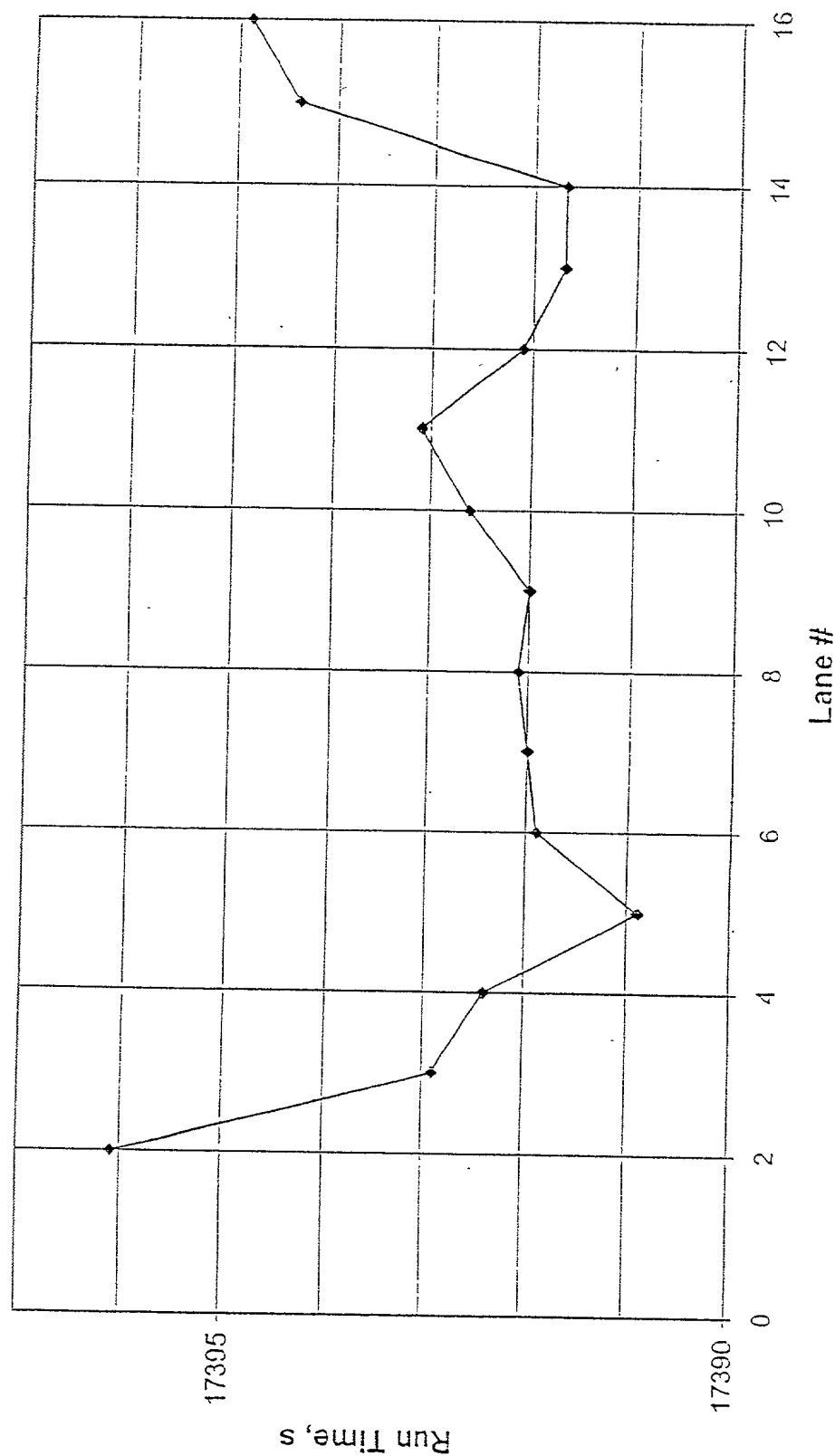


Figure 5

RT-PCR amplicon (1.3 kbp)

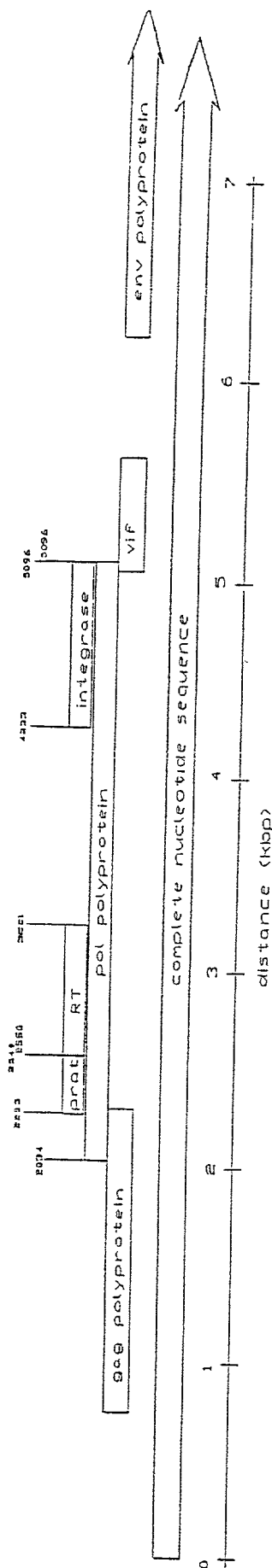
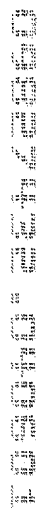


Figure 6



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 7

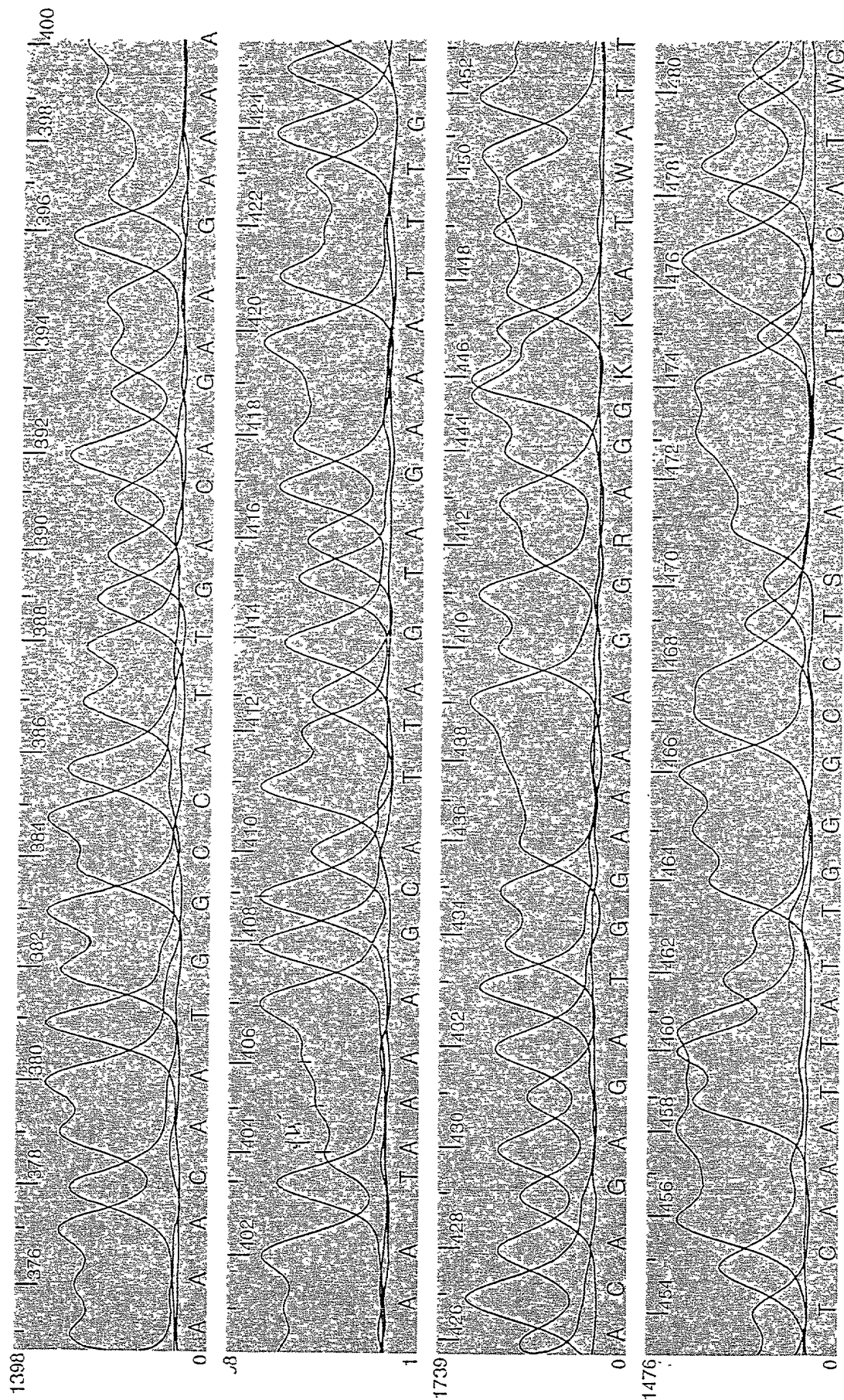




Figure 9A

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

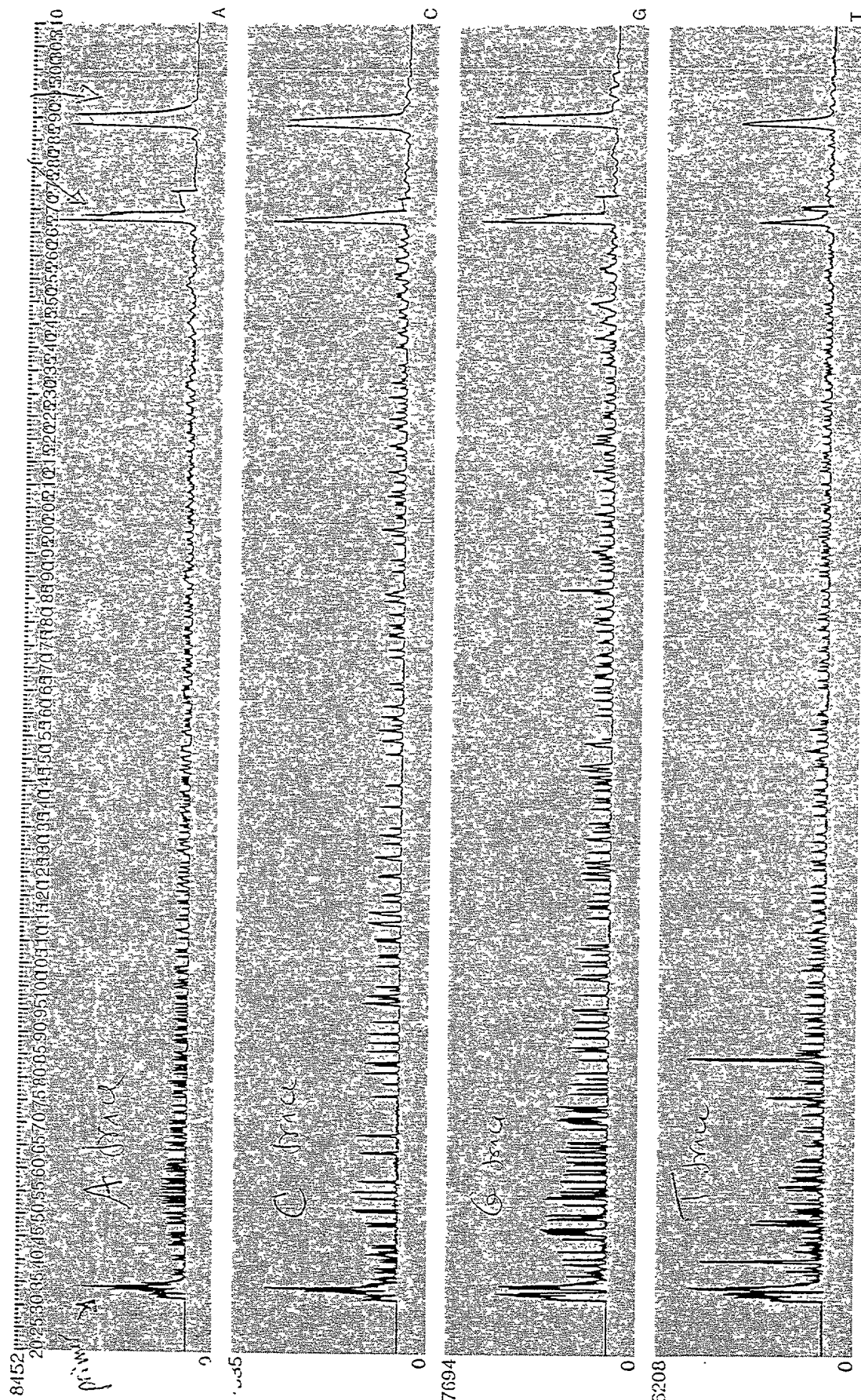
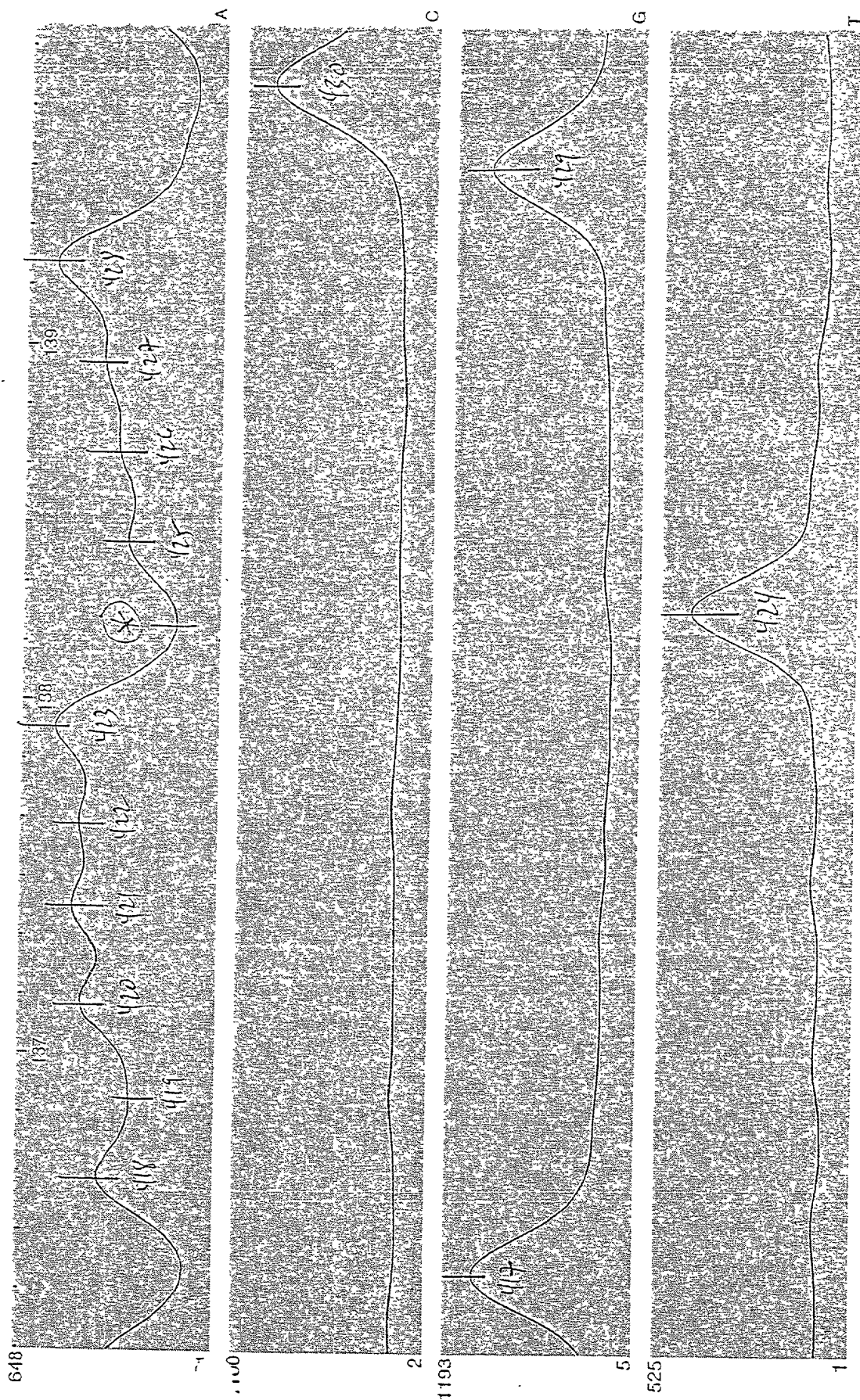




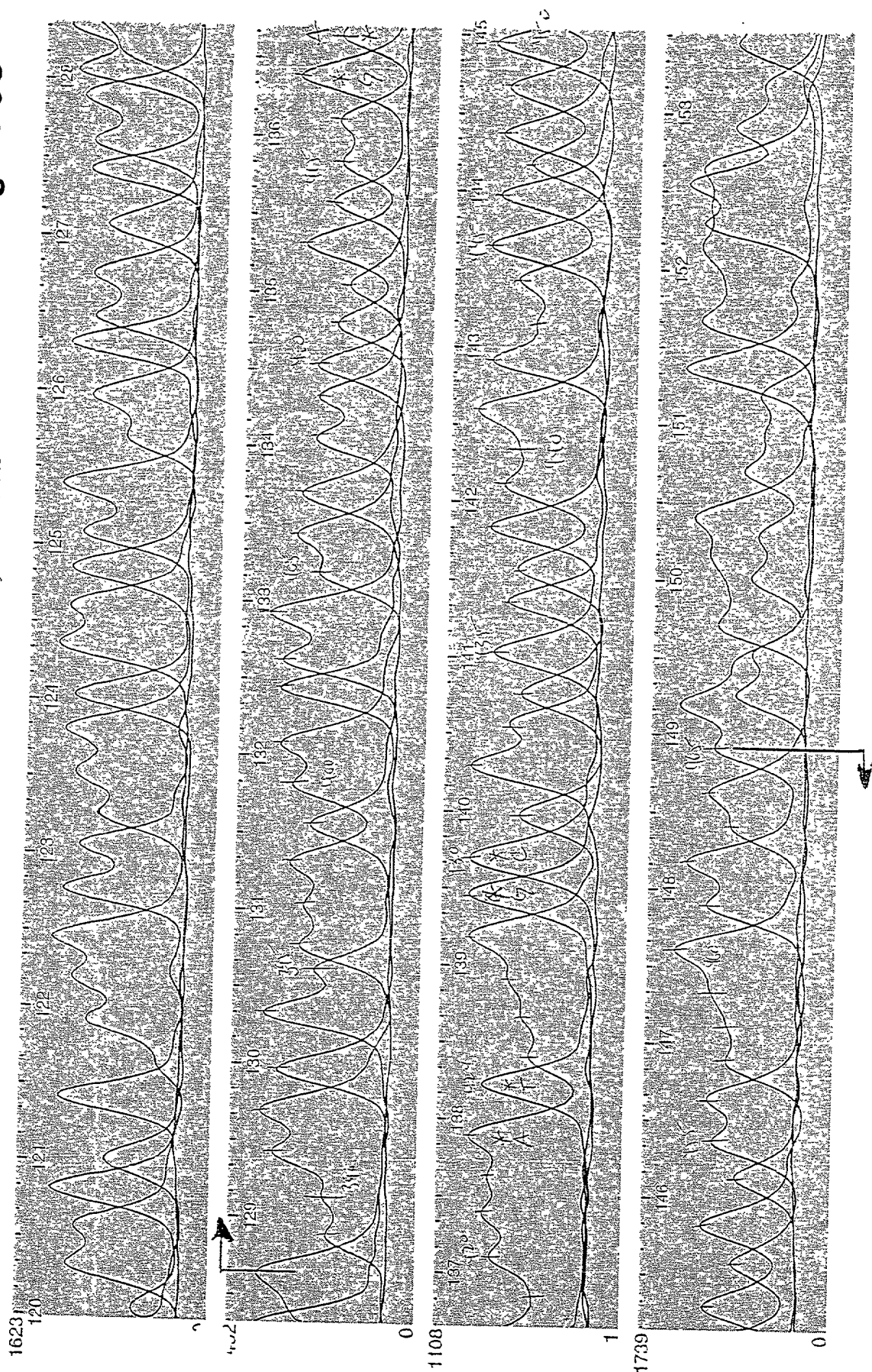
Figure 9B





Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 9C



Deviation of the peak position (in number of bases) from the average
as a function of base number in different traces before alignment

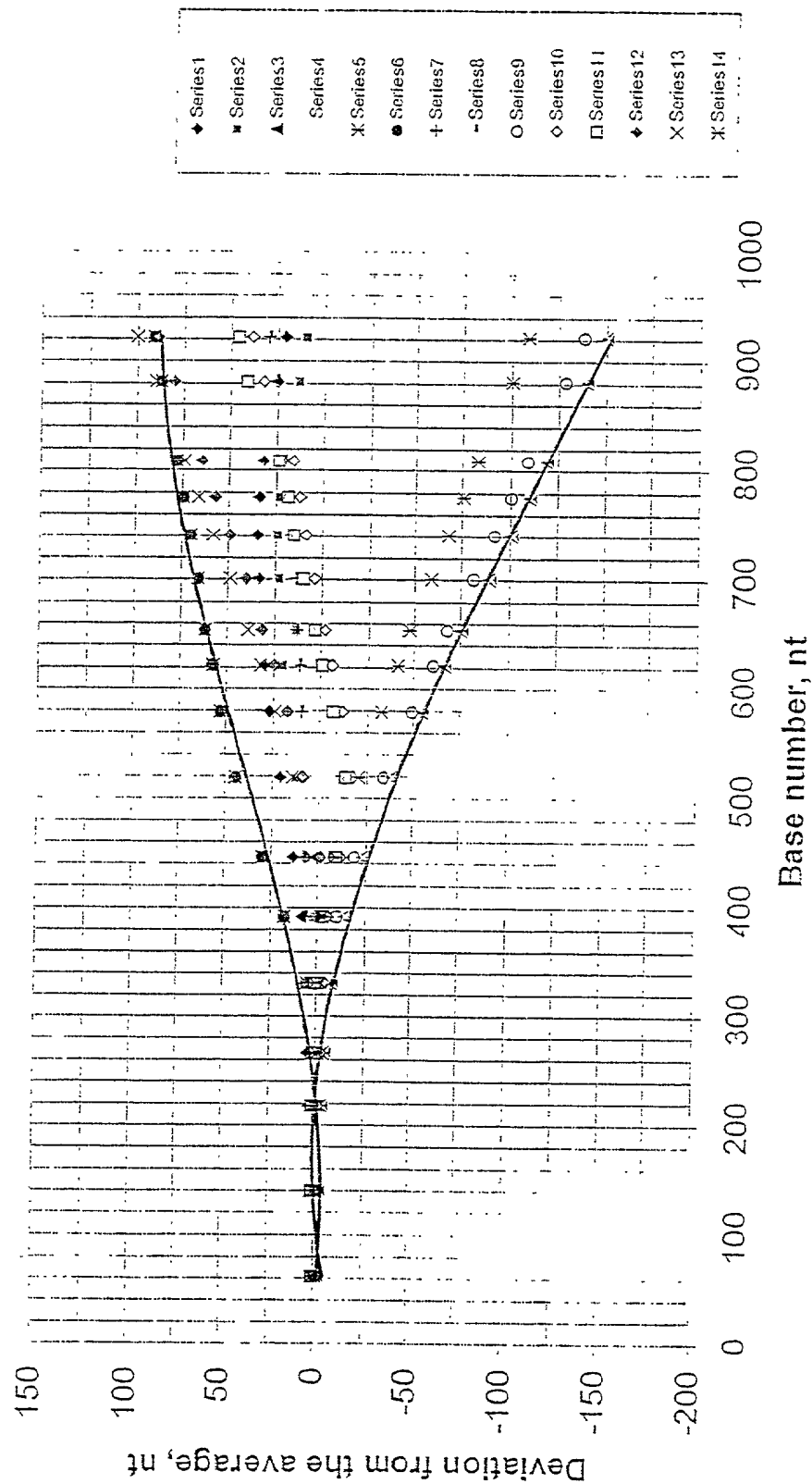


Figure 10

Deviation of the peak position (in number of bases) from the average
as a function of base number in the traces aligned with internal
standards
(long gel, M13, 5-th degree polynomial) 17 ref. peaks

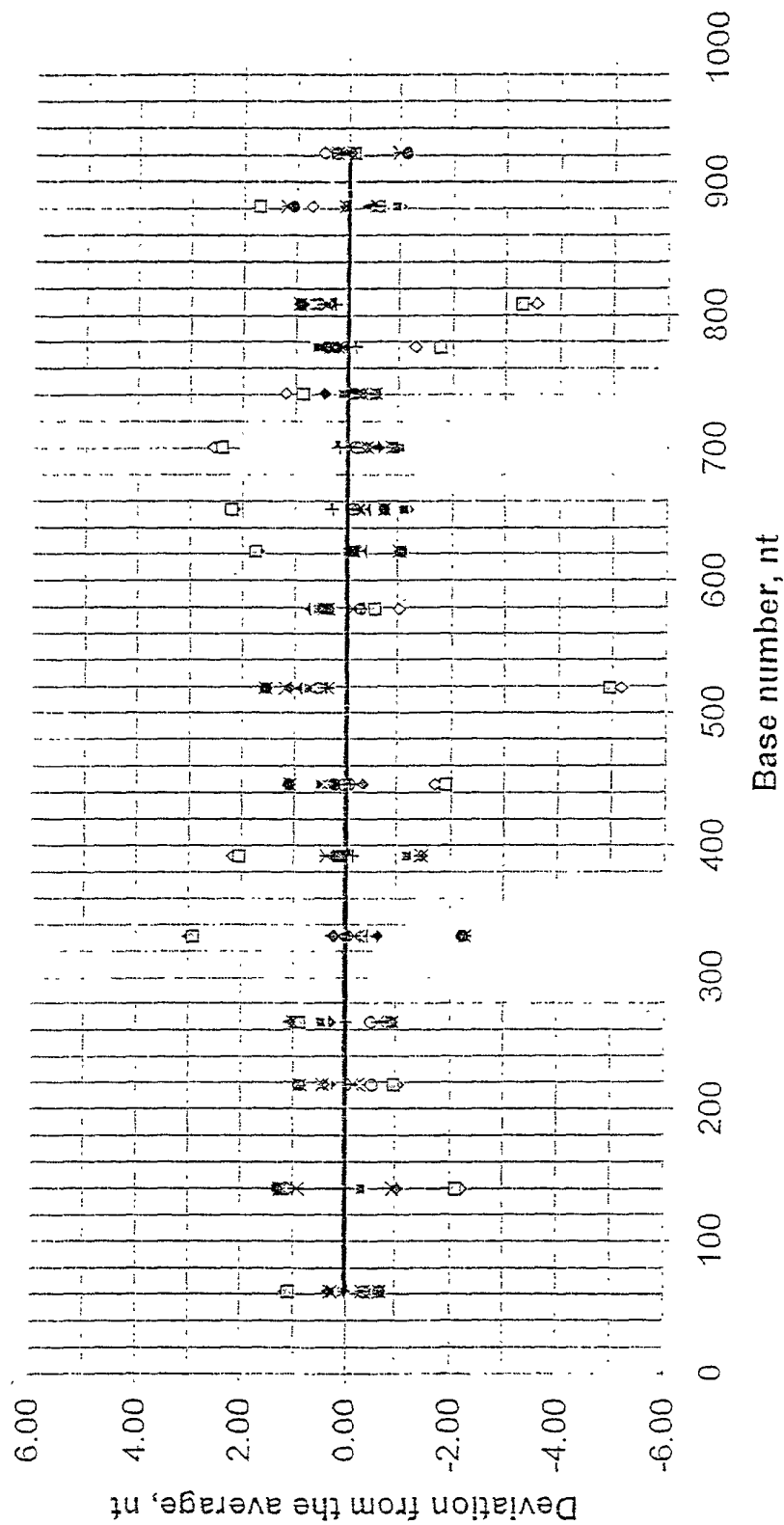


Figure 11

